



# Search Report

EIC 1600

STIC Database Tracking Number: 240590

To: BAO LI  
Location: REM-3D24 / Mailbox 3C18  
Art Unit: 1648  
Thursday, October 18, 2007  
  
Case Serial Number: 10/789355

From: TOBY PORT  
Location: EIC 1600  
REM-1D58 / REM-1A59  
Phone: (571)272-2523  
  
[toby.port@uspto.gov](mailto:toby.port@uspto.gov)

## Search Notes

Dear Examiner LI:

Enclosed are the results for the alignment portion of your sequence search. The results for Seq ID 30 translated and edited should be in SCORE on Monday. If you have any questions, please don't hesitate to call me.

Thank you for using STIC search services.

Toby Port  
x22523









5461	b	Db	5520	AATGGAGAGTGGCTTAACCTCCCTAATGAAAGGAATGCGAAC	5541	Db	5520	CGGCCCCCGCAGCCCTCCGGCCAATTATTCAGGGCTGTGGGGCTGCGAAC	6660
5521	y	Qy	5580	ATTCAACAGAAGGCAATGGTTGCTGAAACAGCCACCAAGGCAAGGCGCTG	6601	Db	5580	CTGAGGATAGTGGAGGCTGCTGGGATTCAGTCAAGAGTGTGATG	6720
5521	b	Db	5580	ATTCAACAGAAGGCAATGGTTGCTGAAACAGCCACCAAGGCAAGGCGCTG	6661	Qy	5580	CTGACAACCTAAAGCTGCCCTGCAAGGTTGGGCCCCGAAATTCTCACAGAAAGTGTGATG	6780
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Accession	Description	Length	Strand	Organism
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			Dy	VERSION
			Db	complete genome; core protein: glycoprotein E1; glycoprotein E2;
			Dy	NS2 protease/he liase; NS3 protease; NS4A protease
			Db	cofactor; NS4B protein; NS5A phosphoprotein; NS5B RNA dependant RNA
			Dy	polymerase; P7 peptide; polypeptide.
			Db	Hepatitis C virus subtype 1b
			Dy	Hepatitis C virus subtype 1b
			Db	Hepatitis C virus
			Dy	ORGANISM
			Db	SOURCE

**Viruses** **sRNA positive-strand viruses, no DNA stage; Flaviviridae;**  
Hepacivirus.

1 Lohmann, V., Korner, F., Koch, J., Herian, U., Theilmann, I. and

Bartenschlager, R.  
Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell

JOURNAL  
Science 285 (5424), 110-113 (1999)  
PUBLISHED 10390360  
REFERENCE 2 (bases 1 to 9605)  
AUTHORS Bartenschlager, R.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAY-1999) Bartenschlager R., Institute for Virology,  
Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67,  
55131 Mainz, GERMANY

## FEATURES

## source

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## 5' UTR

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Search completed: October 18, 2007, 17:20:14  
Job time : 6 secs

GenCore version 6.2.1  
(c) 1993 - 2007 Biocceleration Ltd.

Copyright October 18, 2007, 17:16:54 ; Search time 9 Seconds  
Run on: (without alignments)  
OM nucleic - protein search, using frame\_plus\_n2p model  
4.698 Million cell updates/sec

Title: US-10-789-355A-30  
Perfect score: 17788  
Sequence: 1 gccggccccgattggggc.....ggccctctcgagatcaagt 9605

Scoring table: BLASTN62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Pgapop 6.0 , Fgapext 7.0  
Dgap 6.0 , Delett 7.0

Searched: 1 seqs, 2201 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O=seq10-seq4.res -SINRANGE=0.05 -MINM=0.1 -LOOPEXT=0
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-DOALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -NODEB=LOCAL
-OUTFORMAT=PCL -NORM=ext -HEAPSIZE=0 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6
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Database : seq4.pep : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Query Score	Match Length	DB ID	Description	
- 1	11571	65.0	2201 1	US-10-789-355A-4	Sequence 4, Appli
c 2	131.5	0.7	2201 1	US-10-789-355A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1	Query	Score	Match	Length	DB	ID	Description
US-10-789-355A-4							
; Sequence 4, Application							US/10789355A
; GENERAL INFORMATION:							
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.							
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM							
; TITLE OF INVENTION: HEPATITIS C VIRUS							
; TITLE REFERENCE: 13/083-3-D2							
; CURRENT APPLICATION NUMBER: US/10/789, 355A							
; CURRENT FILING DATE: 2004-02-27							
; PRIOR APPLICATION NUMBER: 60/257, 857							
; PRIOR FILING DATE: 2000-12-22							
; PRIOR APPLICATION NUMBER: 10/029, 907							
; PRIOR FILING DATE: 2001-12-21							
; NUMBER OF SEQ ID NOS: 30							

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Qy	3789	GGGAGCTACTCTCCCAGGCCGCTCCCTCGGCTACTTGAGGGCTCTGGGCTTC	3848
Db	341	GlySerLeuUserProArgProvalSerTyrLeuLySGlyProLeu	360
Qy	3849	CTCTGCCCCCTGGGCAACGCTGGGATCTGGGATCTGGGCTGCGCTGCGT	3908
Db	361	LeuCysProSerGlyHisIalaValAglYilePheArgAlaAlaValCysThrArgIlyVal	380
Qy	3909	GCGAGGGGGGGGAGACTTGTGACCCGTCGAGTCAGTCTATGAAAACCACTATGCGTCCCGGTC	3968
Db	381	AlaLysAlaValAspPheValProValGluSerMetGluThrPheMetArgSerProVal	400
Qy	3969	TTCACGGACAACACTCGTCCTCGGCCCTCGGCCCTACCCAGACATTCCAGGTGACATCTACAC	4028
Db	401	PheThrAspSerSerProAlaValProGlnThrPheGlnValAlaHisLeuHis	420
Qy	4029	GCCCTACTGTTAGGCAAGGACTAACTAGGTCCTGGCTGCGTGTGACGCCAAGGTAT	4088
Db	421	AlaProThrGlySerGlySerGlyLysSerThrLysSvaProAlaAlaAlaLysGlyTyr	440
Qy	4089	AAGGGCTCTGTCCTGAAACCCGTCGGTCCGCCACCTAGGTTGGGGCGTATAATGTC	4148
Db	441	LysValLeuAlaLeuAlaProSerAlaAlaLysGlyLysGlyLysGlyLysSerTyrMetSer	460
Qy	4149	AAGGCACATGCTATGACCTACATCGAACCGGGTAGGACCATCACCGGCTGGCC	4208
Db	461	LysAlaHisGlyIleAspProAsnIleLysGlyLysValArgThrTyrIleThrCysLysAla	480
Qy	4209	CCCATACGTAATCCACCTATGCCAAGTTCTGCGACGGTGGTGTGGGGGGGCC	4268
Db	481	ProIleThrSerThrTyrGlyLysPheLeuAlaAbpGlyGlyCysSerGlyIlyAla	500
Qy	4269	TATGACATCATATAATGATGATGTCGCCACTCAACTGACTCGACCACTATCCTGGC	4328
Db	501	TyrAspIleIleIleCysBspGlyCysIleSerThrAspSerThrIleLeuGlyIle	520
Qy	4329	GGCACAGTCTCTGGACCAAGGGAGACGGCTGGAGCCACTGGGCGACTCGTGCTG	4388
Db	521	GlyThrValleAspGlnAlaGluIthraAlaGlyAlaArgLeuValAlaLeuUserSer	560
Qy	4449	ACTGGAAAATCCCTTTATGCCAAAGCCATCCGACCATCAAGGGGGGAGGG	4508
Db	561	ThrGlyIuleProPheTerGlyIlysValLeuProIleLeuIleGlyIlysGlyIarg	580
Qy	4509	CACCTCATTTCTGCCATTCCAGAAAGAAATGCTGATGAGCTCGCGGAAGGCTGTCGGGC	4568
Db	581	HisLeuIlePheCysHisSerIleProIleSerIleLeuIleGlyIlysLeuSerGly	600
Qy	4569	CTGGAACTCAATGCTGAGCATATTACCGGGCTTGTGATGATCCGGCTATCCA	4628







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Qy 3467 G 3467  
Db 2036 t 2036

Search completed: October 18, 2007, 17:17:24  
Job time : 24.5 SECS





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US-10-789-355A-30 (1-9605) US-10-789-355A-1 Sequence 1 Application US/10789355A

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Initial Score = 6838 Optimized Score = 7416 Significance = 96% Matches = 2625 Misses = 0

Constitutive Substitutions = 98  
Constitutive Interactions = 98

890 888 880 870 860

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GGC

930 940 950 960 970

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THE JOURNAL OF CLIMATE

ACACTCACCATTAGATCACCTCCCCCTGTAGGAACCTAC:GTCCTTACGGAGAA

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1000 1010 1020 1030 1040 1

C A G G A T C A T G C A T A C C C G G G | G C C | C G G T | C G G G A A C A A C T C T

THE STATE OF KENYA

100      110      120      130      140

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10/0 1080 1090 1100 1110 1120  
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170      180      190      200      210

1140 1150 1160 1170 1180 1

-----TGGGGGGGCTGCTCTGCTCCGCTATGTACGTGGAGATCTCTGCGGA-----

卷之三

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AGCTGTACCCCTCGCTCCGGACGACGAGTACAGGACTGCAATTGCTCAATATTCGCCGACG						
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310	320	330	340	350	360	370
1280	1290	1300	1310	1320	1330	1340
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380	390	400	410	420	430	440
1360	1370	1380	1390	1400	1410	1420
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1430	1440	1450	1460	1470	1480	1490
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1510	1520	1530	1540	1550	1560	1570
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1570	1580	1590	1600	1610	1620	1630
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1640	1650	1660	1670	1680	1690	1700
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710	720	730	740	750	760	770
1710	1720	1730	1740	1750	1760	1770
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780	790	800	810	820	830	840
1790	1800	1810	1820	1830	1840	1850
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850	860	870	880	890	900	910
1860	1870	1880	1890	1900	1910	1920
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920	930	940	950	960	970	980
1930	1940	1950	1960	1970	1980	1990
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960	990	1000	1010	1020	1030	1040
2000	2010	2020	2030	2040	2050	2060
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2070	2080	2090	2100	2110	2120	2130

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 1990

GGGGAGCTACTCCCCAGGCCGTTCTACTTGAAAGGGCTTTCGGGCGGTCACTTGCTCTGCCCT	2830	2840	2850	2860	2870	2880	2890	3690	3700	3710	3720	3730	3740	3750
CGGGCACGTGTCGCTATCTTCGGCTGGCAGACCCGAGGGTTCGAAGGGGGACTTTTGATAC	3860	3870	3880	3890	3900	3910	3920	4730	4740	4750	4760	4770	4780	4790
CGGGCACGTGTCGCTATCTTCGGCTGGCAGACCCGAGGGTTCGAAGGGGGACTTTTGATAC	2900	2910	2920	2930	2940	2950	2960	3760	3770	3780	3790	3800	3810	3820
CGGTGAGTCATGAGCTATGAGAACCTATGCGGTCGGCATCTTCGGCTGGCAGACCCGAGGG	3940	3950	3960	3970	3980	3990	4000	4800	4810	4820	4830	4840	4850	4860
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AGACATTCCAGGCTATAGGTGCTTCTACAGGCCCTACTTGAGGGCAAGAGCACTAACTGCGATATG	3040	3050	3060	3070	3080	3090	3100	3910	3920	3930	3940	3950	3960	3970
CAGGCCAAGGCTATAAGGTGCTTCTACAGGCCCTACTTGAGGGCAAGAGCACTAACTGCGATATG	4080	4090	4100	4110	4120	4130	4140	4940	4950	4960	4970	4980	4990	5010
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CGGCCACTTCTGGCTGGCACTGGGAGGGTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	3400	3410	3420	3430	3440	3450	3460	4190	4200	4210	4220	4230	4240	4250
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GGCACCTTCTGGCTGGCACTGGGAGGGTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	4510	4520	4530	4540	4550	4560	4570	5380	5390	5400	5410	5420	5430	5440
GGCACCTTCTGGCTGGCACTGGGAGGGTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	3550	3560	3570	3580	3590	3600	3610	4410	4420	4430	4440	4450	4460	4470
ATGCTGTAATGGGCGCTTCTGGTATCTGGTATCTGGTATCTGGTATCTGGTATCTGGTATCTGGT	4580	4590	4600	4610	4620	4630	4640	5480	5490	5500	5510	5520	5530	5540
ATGCTGTAATGGGCGCTTCTGGTATCTGGTATCTGGTATCTGGTATCTGGTATCTGGTATCTGGT	3620	3630	3640	3650	3660	3670	3680	4480	4490	4500	4510	4520	4530	4540
CGGACCTTCTGGCTGGCACTGGGAGGGTCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG	4660	4670	4680	4690	4700	4710	4720	4550	4560	4570	4580	4590	4600	4610

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7430 7440 7450 7460 7470 7480 7490  
8470 8480 8490 8500 8510 8520 8530  
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7510 7520 7530 7540 7550 7560 7570  
8540 8550 8560 8570 8580 8590 8600  
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7580 7590 7600 7610 7620 7630 7640  
8620 8630 8640 8650 8660 8670 8680  
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7650 7660 7670 7680 7690 7700 7710  
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8760 8770 8780 8790 8800 8810 8820  
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8830 8840 8850 8860 8870 8880 8890  
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7870 7880 7890 7900 7910 7920 7930  
8900 8910 8920 8930 9000 9010 9040  
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8010 8020 8030 8040 8050 8060 8070  
9050 9060 9070 9080 9090 9100 9110  
TCATACTCTGGACAGGGTCAAGGAAACTGGCTGAATGCTGAGTTCTGCTGAGACATCCGGCGAA  
|||||||





3720	3730	3740	3750	3760	3770	3780	4580	4590	4600	4610	4620	4630	4640
CGGCAGCTGGACCTTAACTTGTCAAGGAGATGCCATGTCATTCCGGCTGGCGGCGACGGCAG	CGGCAGCTGGACCTTAACTTGTCAAGGAGATGCCATGTCATTCCGGCTGGCGGCGACGGCAG	CGGCAGCTGGACCTTAACTTGTCAAGGAGATGCCATGTCATTCCGGCTGGCGGCGACGGCAG	TGCTGTAGCATATACTCGGGCTTGATGTTATCCGTCATACATGGAGACTGTCATCATGGTCAAC	TGCTGTAGCATATACTCGGGCTTGATGTTATCCGTCATACATGGAGACTGTCATCATGGTCAAC	TGCTGTAGCATATACTCGGGCTTGATGTTATCCGTCATACATGGAGACTGTCATCATGGTCAAC	TGCTGTAGCATATACTCGGGCTTGATGTTATCCGTCATACATGGAGACTGTCATCATGGTCAAC	3620	3630	3640	3650	3660	3670	3680
2750	2760	2770	2780	2790	2800	2810	4660	4670	4680	4690	4700	4710	4720
GGGAGCCACTACTCTCCCAGGCCCGTCTCTTCACTTGAAGGGCTCTGGCGCTTCACTGGCTCTGC	GGGAGCCACTACTCTCCCAGGCCCGTCTCTTCACTTGAAGGGCTCTGGCGCTTCACTGGCTCTGC	GGGAGCCACTACTCTCCCAGGCCCGTCTCTTCACTTGAAGGGCTCTGGCGCTTCACTGGCTCTGC	GGACCGCTCTCATATGAGGGCTTTAACGGGATATTGAGCTATGATGTCATGAGCTGACCGCTAAC	GGACCGCTCTCATATGAGGGCTTTAACGGGATATTGAGCTATGATGTCATGAGCTGACCGCTAAC	GGACCGCTCTCATATGAGGGCTTTAACGGGATATTGAGCTATGATGTCATGAGCTGACCGCTAAC	GGACCGCTCTCATATGAGGGCTTTAACGGGATATTGAGCTATGATGTCATGAGCTGACCGCTAAC	3650	3660	3670	3680	3690	3700	3710
3790	3800	3810	3820	3830	3840	3850	4730	4740	4750	4760	4770	4780	4790
GGGGAGCTACTCTCCCAGGCCCGTCTCTTCACTTGAAGGGCTCTGGCGCTTCACTGGCTCTGC	GGGGAGCTACTCTCCCAGGCCCGTCTCTTCACTTGAAGGGCTCTGGCGCTTCACTGGCTCTGC	GGGGAGCTACTCTCCCAGGCCCGTCTCTTCACTTGAAGGGCTCTGGCGCTTCACTGGCTCTGC	AGTCGACTCTCGGCGACCTTCACCATGGAGCTGACCGCTAACGGGCTCTGGCTCTGC	AGTCGACTCTCGGCGACCTTCACCATGGAGCTGACCGCTAACGGGCTCTGGCTCTGC	AGTCGACTCTCGGCGACCTTCACCATGGAGCTGACCGCTAACGGGCTCTGGCTCTGC	AGTCGACTCTCGGCGACCTTCACCATGGAGCTGACCGCTAACGGGCTCTGGCTCTGC	3760	3770	3780	3790	3800	3810	3820
2830	2840	2850	2860	2870	2880	2890	4740	4750	4760	4770	4780	4790	4800
GGGGAGCTGCTGGGGATCTTGGGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	GGGGAGCTGCTGGGGATCTTGGGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	GGGGAGCTGCTGGGGATCTTGGGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	GGAGGGCGAGGCGACCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	GGAGGGCGAGGCGACCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	GGAGGGCGAGGCGACCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	GGAGGGCGAGGCGACCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG	3830	3840	3850	3860	3870	3880	3890
2900	2910	2920	2930	2940	2950	2960	4800	4810	4820	4830	4840	4850	4860
CGTGAGTCTATGGAAACCACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	3870	3880	3890	3900	3910	3920	3930						
3940	3950	3960	3970	3980	3990	4000	4870	4880	4890	4900	4910	4920	4930
CGTGAGTCTATGGAAACCACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CGTGAGTCTATGGAAACCACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CGTGAGTCTATGGAAACCACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	GGGCGATGTTACGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	GGGCGATGTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	GGGCGATGTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	GGGCGATGTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	3920	3930	3940	3950	3960	3970	3980
3010	3020	3030	3040	3050	3060	3070	4940	4950	4960	4970	4980	4990	5000
GACATTCAGGGCTTACGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	GACATTCAGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	GACATTCAGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CGAGACCTCTGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CGAGACCTCTGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CGAGACCTCTGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CGAGACCTCTGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	3990	4000	4010	4020	4030	4040	4050
4010	4020	4030	4040	4050	4060	4070	5020	5030	5040	5050	5060	5070	5080
TAAGGGCACATGGTATAAGGTGCTTCCTAACCTGGCTTACGGGAGCACTAAGGTCGGCGAGAC	TAAGGGCACATGGTATAAGGTGCTTCCTAACCTGGCTTACGGGAGCACTAAGGTCGGCGAGAC	TAAGGGCACATGGTATAAGGTGCTTCCTAACCTGGCTTACGGGAGCACTAAGGTCGGCGAGAC	CTGGGAGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CTGGGAGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CTGGGAGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	CTGGGAGGGCTTACGGGAGCACTAAGGTCGGCGAGACACTCTGG	4050	4060	4070	4080	4090	4100	4110
3080	3090	3100	3110	3120	3130	3140	4080	4090	4100	4110	4120	4130	4140
AGCCCAGGGTATAAGGTGCTTCCTAACCTGGCTTACGGGAGCACTAAGGTCGGCGAGAC	AGCCCAGGGTATAAGGTGCTTCCTAACCTGGCTTACGGGAGCACTAAGGTCGGCGAGAC	AGCCCAGGGTATAAGGTGCTTCCTAACCTGGCTTACGGGAGCACTAAGGTCGGCGAGAC	5090	5100	5110	5120	5130	5140	5150	5160	5170	5180	5190
3150	3160	3170	3180	3190	3200	3210	4150	4160	4170	4180	4190	4200	4210
3150	3160	3170	3180	3190	3200	3210	4210	4220	4230	4240	4250	4260	4270
4150	4160	4170	4180	4190	4200	4210	5160	5170	5180	5190	5200	5210	5220
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3220	3230	3240	3250	3260	3270	3280	4220	4230	4240	4250	4260	4270	4280
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3330	3340	3350	3360	3370	3380	3390	4240	4250	4260	4270	4280	4290	4300
4330	4340	4350	4360	4370	4380	4390	5230	5240	5250	5260	5270	5280	5290
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3440	3450	3460	3470	3480	3490	3500	5300	5310	5320	5330	5340	5350	5360
GCGCACTCACTGACTGCAACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGAC	GCGCACTCACTGACTGCAACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGAC	GCGCACTCACTGACTGCAACTATGGGGCTTACGGGAGCACTAAGGTCGGCGAGAC	GGAGGTGTCAGGAGGTTACGGGAGCACTAAGGTCGGCGAGAC	GGAGGTGTCAGGAGGTTACGGGAGCACTAAGGTCGGCGAGAC	GGAGGTGTCAGGAGGTTACGGGAGCACTAAGGTCGGCGAGAC	GGAGGTGTCAGGAGGTTACGGGAGCACTAAGGTCGGCGAGAC	4410	4420	4430	4440	4450	4460	4470
3540	3550	3560	3570	3580	3590	3600	5450	5460	5470	5480	5490	5500	5510

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 5520 5530 5540 5550 5560 5570 5580  
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 5590 5600 5610 5620 5630 5640 5650  
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GAAGGACCCGAACTACGTCCTCCAGTGTAACAGGTTGTCATTGCGCCCTCAGGCCCTCCGATAC 7250 7260 7270 7280 7290 7300 7310	8110 8120 8130 8140 8150 8160 8170
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7540 7550 7560 7570 7580 7590 7600	8400 8410 8420 8430 8440 8450 8460
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7610 7620 7630 7640 7650 7660 7670	8470 8480 8490 8500 8510 8520 8530
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GAGCAACTCTTGTCTGGCTCACACACTTGGCTTACATGCACTGGCTGGGAGGA 6710 6720 6730 6740 6750 6760 6770	8540 8550 8560 8570 8580 8590 8600 8610
7680 7690 7700 7710 7720 7730 7740	CCTTGCGGAGGACGACCCGCTGTTGAAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7580 7590 7600 7610 7620 7630 7640
GAGCAACTCTTGTCTGGCTCACACACTTGGCTTACATGCACTGGCTGGGAGGA 6790 6800 6810 6820 6830 6840 6850	8620 8630 8640 8650 8660 8670 8680
7750 7760 7770 7780 7790 7800 7810	CTTCAGGAGGCTTGTAGATGATCTCTGGGACCCCTGGGAGGAGGAGGAGGAGGAGG 7650 7660 7670 7680 7690 7700 7710
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7920 7930 7940 7950 7960 7970 7980	8760 8770 8780 8790 8800 8810 8820
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 9340 9350 9360 9370 9380 9390 9400  
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 9410 9420 9430 9440 9450 9460 9470  
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 Aps保守性 Substitutions = 98  
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-TTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
500 510 520 530 540 550 560

1500 1510 1520 1530 1540 1550 1560  
CTATGTGACAGGGGGGACATGGCCAAAACACCTCTGGGATTCGCTCTCTCT  
CTGGAGGAGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
570 580 590 600 610 620 630

1570 1580 1590 1600 1610 1620 1630  
GAATTCAGCGCTTGTAAACCAACAGGAGCTGCTGCTGCTGCTGCTGCTGCT  
GTCCTGAGGCCGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
640 650 660 670 680 690 700

1640 1650 1660 1670 1680 1690 1700 1710  
CAACACTGGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
GCTCTGCGGAGAGAGTATCCATGCTGGTGTGCTGCTGCTGCTGCTGCT  
710 720 730 740 750 760 770

6. US-10-789-355A-30 (1-9605)  
US-10-789-355A-6 Sequence 6, Application US/10789355A

Initial Score = 6821	Optimized Score = 7399	Significance = 1.37
Residue Identity = 86%	Matches = 7508	Mismatches = 114
Gaps = 98	Conservative Substitutions = 0	



TACGGCCCTACTCCGAAACAGCGGAGCCCTACTTGGCATCATACATTGGCTCAGGGCGGGAGAAGAA	2470	2480	2490	2500	2510	2520	2530	3330	3340	3350	3360	3370	3380	3390
3500 3510 3520 3530 3540 3550 3560 3570	3580	3590	3600	3610	3620	3630	3640	4370	4380	4390	4400	4410	4420	4430
CCAGGTGAGGGGGAGGTTCAAGTGGTCTTCACCGGAACACAAATCTTCCTGGAGACCTGGCTCAATGGCT	3540	3550	3560	3570	3580	3590	3600	3410	3420	3430	3440	3450	3460	3470
CCAGGTGAGGGGGAGGTTCAAGTGGTCTTCACCGGAACACAAATCTTCCTGGAGACCTGGCTCAATGGCT	2540	2550	2560	2570	2580	2590	2600	3410	3420	3430	3440	3450	3460	3470
4440 4450 4460 4470 4480 4490 4500	4510	4520	4530	4540	4550	4560	4570	4510	4520	4530	4540	4550	4560	4570
GTCGTGCTGTCATCATGTCGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTCATGTCGTC	3610	3620	3630	3640	3650	3660	3670	3480	3490	3500	3510	3520	3530	3540
3680 3690 3700 3710 3720 3730 3740 3750	3760	3770	3780	3790	3800	3810	3820	3610	3620	3630	3640	3650	3660	3670
CACCAATGTCGACCGGGACCCCTTGTCGGTCAAGAGCCCTTCCTTGACCATGCACTG	2610	2620	2630	2640	2650	2660	2670	3550	3560	3570	3580	3590	3600	3610
CACCAATGTCGACCGGGACCCCTTGTCGGTCAAGAGCCCTTCCTTGACCATGCACTG	2680	2690	2700	2710	2720	2730	2740	3610	3620	3630	3640	3650	3660	3670
4580 4590 4600 4610 4620 4630 4640 4650	4660	4670 4680	4690	4700	4710	4720	4730	4660	4670	4680	4690	4700	4710	4720
TGCGTAGCATATTACCGGGCTTCCTTGATCTCGGTATCGGTATCGGTATCGGTATCGGTATCGGTATCGGT	3710	3720	3730	3740	3750	3760	3770	3710	3720	3730	3740	3750	3760	3770
3780 3790 3800 3810 3820 3830 3840 3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990
GGGGAGCCCTACTCTCCGACGGCCCTTCCTACTTGAAAGGGCTCTCCACTCTGCGCC	2830	2840	2850	2860	2870	2880	2890	3930	3940	3950	3960	3970	3980	3990
GGGGAGCCCTACTCTCCGACGGCCCTTCCTACTTGAAAGGGCTCTCCACTCTGCGCC	2900	2910	2920	2930	2940	2950	2960	3930	3940	3950	3960	3970	3980	3990
4810 4820 4830 4840 4850 4860	4870	4880	4890	4900	4910	4920	4930	4810	4820	4830	4840	4850	4860	4870
GCACGGCGCAAGGGAGCTGGCTTCCTGGCTTGGGGATGGCGATTAGCGCTTGGCTTGGCTTGGCTTGGCT	3940	3950	3960	3970	3980	3990	4000	3760	3770	3780	3790	3800	3810	3820
CGTCAGTCATGTCGATCTGGCTTCCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	2970	2980	2990	3000	3010	3020	3030	3930	3940	3950	3960	3970	3980	3990
4930 4940 4950 4960 4970 4980 4990 5000	5010	5020	5030	5040	5050	5060	5070	5090	5110	5120	5130	5140	5150	5160
GACATTCAGGTATAAGGTGTTGTCCTGAACTACCCCTACTGGCTTCAGGCAAGGCACTAACAGGTGCTGCCATATGCA	4010	4020	4030	4040	4050	4060	4070	4940	4950	4960	4970	4980	4990	5000
GACATTCAGGTATAAGGTGTTGTCCTGAACTACCCCTACTGGCTTCAGGCAAGGCACTAACAGGTGCTGCCATATGCA	4080	4090	4100	4110	4120	4130	4140	4940	4950	4960	4970	4980	4990	5000
TAAGGCACTGTTGTCCTGAACTACCCCTACTGGCTTCAGGCAAGGCACTAACAGGTGCTGCCATATGCA	3110	3120	3130	3140	3150	3160	3170	3930	3940	3950	3960	3970	3980	3990
4150 4160 4170 4180 4190 4200 4210 4220	4230	4240	4250	4260	4270	4280	4290	4030	4040	4050	4060	4070	4080	4090
CTCCACCTATGCAAGTTGTCCTGAACTACCCCTACTGGCTTCAGGCAAGGCACTAACAGGTGCTGCCATATGCA	4300	4310	4320	4330	4340	4350	4360	4130	4140	4150	4160	4170	4180	4190
GTGCCACCTACGTTGTCCTGAACTACCCCTACTGGCTTCAGGCAAGGCACTAACAGGTGCTGCCATATGCA	4220	4230	4240	4250	4260	4270	4280	4220	4230	4240	4250	4260	4270	4280

5230 5240 5250 5260 5270 5280 5290  
 AGCGTTCAAAAGGTTACTACACACCCCCATAACCAAATACATGGCATGCAGTCGGTGA  
 AGCGTTCAAAAGGTTACTACACACCCCCATAACCAAATACATGGCATGCAGTCGGTGA  
 4 270 4 280 4 300 4 310 4 320 4 330  
 5300 5310 5320 5330 5340 5350 5360  
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 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 GGAGTCGTCAGGCCACCTGGGTCTGGAGCCGAGTCCTAGCAGCTCTGGCCATGCAG  
 4 340 4 350 4 360 4 370 4 380 4 390 4 400  
 5380 5390 5400 5410 5420 5430 5440  
 AGGAGCGTGCTCATTTGTTGGCAGGATCATTTGTTGGAAAGGCCATCATTCGGCA  
 ||||| ||||| ||||| ||||| ||||| |||||  
 AGGAGCGTGCTCATTTGTTGGCAGGATCATTTGTTGGAAAGGCCATCATTCGGCA  
 4 410 4 420 4 430 4 440 4 450 4 460 4 470  
 5450 5460 5470 5480 5490 5500 5510  
 TTACCGGGACTTCGATGAGTGGAGAAGTGGGCCCTACACCTCCCTAACATCGAA  
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 TTACCGGGACTTCGATGAGTGGAGAAGTGGGCCCTACACCTCCCTAACATCGAA  
 4 480 4 490 4 500 4 510 4 520 4 530 4 540  
 5520 5530 5540 5550 5560 5570 5580  
 CGAAACATTCAACAGAAGGAAATCGGTGAGAAGTGGGCCCTACACCCACCA  
 ||||| ||||| ||||| ||||| |||||  
 TTACCGGGACTTCGATGAGTGGAGAAGTGGGCCCTACACCTCCCTAACATCGAA  
 4 550 4 560 4 570 4 580 4 590 4 600 4 620  
 5590 5600 5610 5620 5630 5640 5650  
 GGTGGAATCCAAGTGGAAACCCCTCGAAGCCTTCTGGCGAGCATAGCGGGATA  
 ||||| ||||| ||||| ||||| |||||  
 GGTGGAATCCAAGTGGAAACCCCTCGAAGCCTTCTGGCGAGCATAGCGGGATA  
 4 630 4 640 4 650 4 660 4 670 4 680 4 690  
 5660 5670 5680 5690 5700 5710 5720  
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 ATATTAGCAGGGCTGCTGCCACTCTGCTGGCAACCCCGCATAGCATGCCTCAT  
 4 700 4 710 4 720 4 730 4 740 4 750 4 760  
 5740 5750 5760 5770 5780 5790 5800  
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 ||||| ||||| ||||| |||||  
 CACCGCCCGCTCACCAACCAATCCCTCGTAAATCCCTCGGCGGATGGCC  
 4 770 4 780 4 790 4 800 4 810 4 820 4 830  
 5810 5820 5830 5840 5850 5860 5870  
 TCCPCCAGGCTGCTGCCACTCTGCTGGCAACCCCGCATAGCATGCCTCAT  
 ||||| ||||| ||||| |||||  
 TCCPCCAGGCTGCTGCCACTCTGCTGGCAACCCCGCATAGCATGCCTCAT  
 4 840 4 850 4 860 4 870 4 880 4 890 4 900  
 5880 5890 5900 5910 5920 5930 5940  
 GAAGGTGCTGTTGGATAATTGGCAGGCTTATGGAGCAGGCTCTGG  
 ||||| ||||| ||||| |||||  
 GAAGGTGCTGTTGGATAATTGGCAGGCTTATGGAGCAGGCTCTGG  
 4 910 4 920 4 930 4 940 4 950 4 960 4 980  
 5950 5960 5970 5980 5990 6000 6010  
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 4 990 5 000 5 010 5 020 5 030 5 040 5 050  
 6020 6030 6040 6050 6060 6070 6080 6090  
 CGTCGGCGCTGCGCAGGATACTCGTGGCACTGCTGGCGGCT  
 ||||| ||||| ||||| |||||  
 CGTCGGCGCTGCGCAGGATACTCGTGGCACTGCTGGCGGCT  
 5 060 5 070 5 080 5 090 5 100 5 110 5 120 5 130  
 6100 6110 6120 6130 6140 6150 6160  
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 CGCGCTATAGGGTCCCTCCGGGTAACCAAGCTCTCCCGGCT  
 5 140 5 150 5 160 5 170 5 180 5 190  
 6170 6180 6190 6200 6210 6220 6230  
 ACCACGCTGTCGACTCAGATCCTCTACTACATCTGCT  
 ||||| ||||| |||||  
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 5 200 5 210 5 220 5 230 5 240 5 250 5 260  
 6240 6250 6260 6270 6280 6290 6300  
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 5 270 5 280 5 290 5 300 5 310 5 320 5 330  
 6310 6320 6330 6340 6350 6360 6370  
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 5 350 5 360 5 370 5 380 5 390 5 400 5 410  
 6380 6390 6400 6410 6420 6430 6440  
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 5 420 5 430 5 440 5 450 5 460 5 470 5 480  
 6460 6470 6480 6490 6500 6510 6520  
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 5 490 5 500 5 510 5 520 5 530 5 540 5 550  
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 CATAAACCGGTTAACCCGCGCCCTGCAAGCGCC  
 5 560 5 570 5 580 5 590 5 600 5 610 5 620  
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 5 630 5 640 5 650 5 660 5 670 5 680 5 690  
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 ||||| |||||  
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 5 710 5 720 5 730 5 740 5 750 5 760 5 770  
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 ||||| |||||  
 CGTCACAGGCTGCAACCCCTCTAGGGAGGCT  
 5 780 5 790 5 800 5 810 5 820 5 830 5 840  
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 GTCAACAGTCCATGGAAGGCTGCACTTCCTG  
 5 850 5 860 5 870 5 880 5 890 5 900 5 910  
 6890 6900 6910 6920 6930 6940 6950  
 TAGCGGGAGGAGGCTAAGCTGCTGGCG  
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 5 920 5 930 5 940 5 950 5 960 5 970 5 980

GCTGTCGCCCCCTCCCTTGAAGGCAACATGACTAACCGCATGACTCCTGGACGCTGACGGC  
GCTGTCGCCCCCTCCCTTGAAGGCAACATGACTAACCGCATGACTCCTGGACGCTGACGGC  
5990 6000 6010 6020 6030 6040 6050 6060  
7030 7040 7050 7060 7070 7080 7090 7090  
CAACCTCCCTGGCGCAGGATGGGGAAACATACCCCGCTGAGTCAGAAAATAAGGTAGTAAATT  
CAACCTCCCTGGCGCAGGATGGGGAAACATACCCCGCTGAGTCAGAAAATAAGGTAGTAAATT  
6070 6080 6090 6100 6110 6120 6130  
7100 7110 7120 7130 7140 7150 7160 7170  
GGACTCTTGTAGGCCCTCCAGGGAGGATGACAAGGAGATTCGTTCCGGAGATCCCTCGGAG  
GGACTCTTGTAGGCCCTCCAGGGAGGATGACAAGGAGATTCGTTCCGGAGATCCCTCGGAG  
6140 6150 6160 6170 6180 6190 6200  
7180 7190 7200 7210 7220 7230 7240 7240  
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GTCCAGGAATTCCCTCGAGGGATGCCCATAACCCCTCCCTGTTAGAGTCCTG  
6210 6220 6230 6240 6250 6260 6270  
7250 7260 7270 7280 7290 7300 7310  
GAAGGACCCGGAACTAGTCCCTCCAGTGTAACAGGGTGTCCATTGGCCCTGCCATTAC  
GAAGGACCCGGAACTAGTCCCTCCAGTGTAACAGGGTGTCCATTGGCCCTGCCATTAC  
6280 6290 6300 6310 6320 6330 6340  
7320 7330 7340 7350 7360 7370 7380  
ACCTCACCGGGAAAGGAGGACGGTTCCTGTCAGAACTTACCGTGCTTCGGCTGGCA  
ACCTCACCGGGAAAGGAGGACGGTTCCTGTCAGAACTTACCGTGCTTCGGCTGGCA  
6350 6360 6370 6380 6390 6400 6410 6420  
7390 7400 7410 7420 7430 7440 7450  
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AAAGACCTCTCGCAAGCTCGGACCTCGAATCGCTGGCCCTCGAGACGCAACCGCCCTC  
6430 6440 6450 6460 6470 6480 6490  
7460 7470 7480 7490 7500 7510 7520 7530  
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6500 6510 6520 6530 6540 6550 6560  
7540 7550 7560 7570 7580 7590 7600  
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TCCCGATCTCGCAAGCTCGGACCTCGAATCGCTGGCCCTCGAGACGCAACCGCCCTC  
6570 6580 6590 6600 6610 6620 6630  
7610 7620 7630 7640 7650 7660 7670  
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GTCCPACACATGGACGGGCTCTGCTGATCACGCCATGGCTGGAGAACAAAGCTGCT  
6640 6650 6660 6670 6680 6690 6700  
7680 7690 7700 7710 7720 7730 7740  
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GAGGCAACTCTTGCCTCGTCAACCACAACTTGTCTAACACATCTCGCAGGAGCTGG  
6710 6720 6730 6740 6750 6760 6770 6780  
7750 7760 7770 7780 7790 7800 7810  
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6790 6800 6810 6820 6830 6840 6850  
7820 7830 7840 7850 7860 7870 7880 7890  
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GGCTCCACAGTTAAGGCTAAACTCTPATCCSTGGAGGAAGGCTGTAAGCTGACGCCAG  
6860 6870 6880 6890 6900 6910 6920  
7900 7910 7920 7930 7940 7950 7960  
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6930 6940 6950 6960 6970 6980 6990  
7970 7980 7990 8000 8010 8020 8030  
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7000 7010 7020 7030 7040 7050 7060  
8040 8050 8060 8070 8080 8090 8100  
CGTCAAACAGAGGGGGCCCAAGCGCTGGCTTATCCGATTTGGGGTTCTGCTGTTCTG  
CGTCAAACAGAGGGGGCCCAAGCGCTGGCTTATCCGATTTGGGGTTCTGCTGTTCTG  
7070 7080 7090 7100 7110 7120 7130  
8110 8120 8130 8140 8150 8160 8170  
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7150 7160 7170 7180 7190 7200 7210  
8180 8190 8200 8210 8220 8230 8240  
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7220 7230 7240 7250 7260 7270 7280  
8260 8270 8280 8290 8300 8310 8320  
ATATGACACCGCTTGTGACTGAGCTTACGGTCACTGAGATGACTTCGGTGTGCT  
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7290 7300 7310 7320 7330 7340 7350  
8330 8340 8350 8360 8370 8380 8390  
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7360 7370 7380 7390 7400 7410 7420  
8400 8410 8420 8430 8440 8450 8460  
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7430 7440 7450 7460 7470 7480 7490  
8470 8480 8490 8500 8510 8520 8530  
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7510 7520 7530 7540 7550 7560 7570  
8540 8550 8560 8570 8580 8590 8600  
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CGTATGCGAGAGACCTGCTGCTTACGCTGGCTTACGCTGGCT  
7580 7590 7600 7610 7620 7630  
8620 8630 8640 8650 8660 8670 8680  
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CTTAGGAGGGCTTACGATGACTGATCTCTGGGACCGGCCAA  
7650 7660 7670 7680 7690 7700 7710  
8690 8700 8710 8720 8730 8740 8750  
GATACATCATGCTCCATGCTGCT  
GGCGTCCACAGTTAAGGCTAAACTCTPATCCSTGGAGGAAGGCTGTAAGCTGACGCCAG





3360 3370 3380 3390 3400 3410 3420  
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CAGGGGAGGGAGATACTCTGGACCGCAGCAAGCTTGA  
2400 2410 2420 2430 2440 2450 2460  
2430 3440 3450 3460 3470 3480 3490  
TA CGGCCTACTCCAAAGACGGAGGCCACTTGGCT  
TAGGGCTACTCTGGACCGCAGCAAGCTTGA  
TAGGGCTACTCTGGACCGCAGCAAGCTTGA  
2470 2480 2490 2500 2510 2520 2530  
2500 3510 3520 3530 3540 3550 3560  
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CCAGGTCAAGGGAGGTCAAGGGAGTCATGGCT  
2550 2560 2570 2580 2590 2600  
3590 3600 3610 3620 3630 3640  
GTTGGACTGTCTATCATGGTCTGGCCAGCAATTC  
GTTGGACTGTCTATCATGGTCTGGCCAGCAATTC  
2610 2620 2630 2640 2650 2660 2670  
2680 2690 2700 2710 2720 2730 2740  
3650 3660 3670 3680 3690 3700 3710  
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2750 2760 2770 2780 2790 2800 2810  
2820 3720 3730 3740 3750 3760 3770 3780  
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2830 2840 2850 2860 2870 2880 2890  
2900 2910 2920 2930 2940 2950 2960  
3860 3870 3880 3890 3900 3910 3920  
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2970 2980 2990 3000 3010 3020 3030  
3940 3950 3960 3970 3980 3990 4000  
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3040 3050 3060 3070 3080 3090 3100  
4010 4020 4030 4040 4050 4060 4070  
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3110 3120 3130 3140 3150 3160 3170 3180  
4080 4090 4100 4110 4120 4130 4140  
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3190 3200 3210 3220 3230 3240 3250  
4220 4230 4240 4250 4260 4270 4280 4290  
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3260 3270 3280 3290 3300 3310 3320 3330  
4300 4310 4320 4330 4340 4350 4360  
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3330 3340 3350 3360 3370 3380 3390  
3430 3440 3450 3460 3470 3480 3490  
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3400 3410 3420 3430 3440 3450 3460  
4440 4450 4460 4470 4480 4490 4500  
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3470 3480 3490 3500 3510 3520 3530  
4510 4520 4530 4540 4550 4560 4570  
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3550 3560 3570 3580 3590 3600 3610  
4580 4590 4600 4610 4620 4630 4640  
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3620 3630 3640 3650 3660 3670 3680  
4660 4670 4680 4690 4700 4710 4720  
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3690 3700 3710 3720 3730 3740 3750  
4730 4740 4750 4760 4770 4780 4790  
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3760 3770 3780 3790 3800 3810 3820  
4800 4810 4820 4830 4840 4850 4860  
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4870 4880 4890 4900 4910 4920 4930  
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4940 4950 4960 4970 4980 4990 5000 5010  
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3970 3980 3990 4000 4010 4020 4030  
5020 5030 5040 5050 5060 5070 5080  
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5090 5100 5110 5120 5130 5140 5150



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GCCTCTGGCCCTTGCGAACATGCGAACACTAACCTGCGGACCTGACCTCATGCA	5990	6000	6010	6020	6030	6040	6050	6860	6870	6880	6890	6900	6910	6920	
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 AAGGACCAAGCTCAAACCTCAACTTCAACTTCAACTTCAACTTCAACTTCAACT  
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 9260 9270 9280 9290 9300 9310 9320  
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 8300 8310 8320 8330 8340 8350 8360  
 9340 9350 9360 9370 9380 9390 9400